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Lot No.	DQA09-1


**CTS** Collaborative Transplant Study

## WORKING INSTRUCTION

### HLA-DQA1\* CTS-PCR-SSP TRAY KIT

#### LOCUS- AND LOT-SPECIFIC MANUAL

To be applied to the following product:

Product No.	Description
127	HLA-DQA1* low resolution CTS-PCR-SSP Tray Kit 

#### 1. Main differences

- **Between Lot DQA09-1 (the current lot) and Lot DQA09-0:**  
The kit was updated to cover new alleles included in the IMGT/HLA Database of January 2018. Deleted and renamed alleles were taken into consideration.

#### 2. Introduction

- Intended use: This kit reveals a low resolution typing of HLA-DQA1\* by the PCR-SSP method.
- Allele coverage IMGT/HLA Sequence Database Release 3.31.0, January 2018.
- This manual is only valid for **Lot No. DQA09-1**.
- This manual should be used together with the Main Manual (General Information) which is the 'Working instruction for the CTS-PCR-SSP **TRAY and MINITRAY KITS**' (Manual No. 100A).

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#### 4. Kit Composition

- Number of PCR primer mixes per test: 11 (10 allele-specific mixes and 1 negative control mix)
- Please note: Well positions E2 - A2, E4 - A4, E6 - A6, E8 - A8, E10 - A10, E12 - A12 are empty!
- Number of tests per tray: 6
- Number of trays per kit: 10
- The primer mixes are aliquoted and dried in thin-walled, blue PCR-Trays.
- PCR buffer: 3.0 ml of Mastermix SSP (without Taq polymerase).

For storage condition, please refer to Section 1 of the 'Working instruction for the CTS-PCR-SSP TRAY and MINITRAY KITS' (Manual No. 100A) supplied along with this product.

#### 5. Materials, Reagents and Equipment not supplied

Please refer to Section 2 of the 'Working instruction for the CTS-PCR-SSP TRAY and MINITRAY KITS' (Manual No. 100A) supplied along with this product.

#### 6. Sample Requirements, PCR and Gel Electrophoresis

Please refer to Section 3 to 6 of the 'Working instruction for the CTS-PCR-SSP TRAY and MINITRAY KITS' (Manual No. 100A) supplied along with this product.

#### 7. Result Evaluation

- Check the approximate size of the PCR product against the Primer Mix Specificity Table (Table 1) to confirm the correct product size.
- Use the Amplification Pattern Tables (Table 2) to make allele assignment. Alternatively, you can use the SCORE Software ([www.IHWG.org](http://www.IHWG.org)) for detailed result interpretation.

#### 8. Interpretation Hints

- The quality and quantity of DNA as well as of the Taq polymerase are extremely crucial factors. If your bands are too weak you might try to adjust these two factors until you obtain optimal results.
- Please also refer to Section 7 of the 'Working instruction for the CTS-PCR-SSP TRAY and MINITRAY KITS' (Manual No. 100A) supplied along with this product.

#### 9. Special notes

HLA-DQA1\*05:04 generates two PCR fragments with Mix 9.

#### 10. Troubleshooting

Please refer to Section 8 of the 'Working instruction for the CTS-PCR-SSP TRAY and MINITRAY KITS' (Manual No. 100A) supplied along with this product.

#### 11. Precaution

Please refer to Material Safety Data Sheet for the CTS-PCR-SSP TRAY and MINITRAY KITS (Manual No. 100B) supplied along with this product.

#### 12. Contact

If you have any particular questions concerning this kit, which are not answered in this or the Main Manual, please do not hesitate to contact me or my coworkers at:

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Hien Tran, M.D.

### 13. Appendix

**Table 1:** Sizes of the PCR products and allele specificities of each **HLA-DQA1\*** CTS-PCR-SSP primer mix (**Lot No. DQA09-1**) based on IMGT/HLA Sequence Database Release 3.31.0, January 2018

Position						Mix	Allele	Serology	Size
H1	H3	H5	H7	H9	H11	Mix 1	DQA1*01:01:01:01-01:01:01:03/01:01:01:05-01:01:03/01:04:01:01-01:05:02/01:07Q/01:12	-	145 bp
G1	G3	G5	G7	G9	G11	Mix 2	DQA1*01:02:01:01-01:03:01:08/01:06/01:08-01:11/01:13-01:16N	-, Null	145 bp
F1	F3	F5	F7	F9	F11	Mix 3	DQA1*01:01:01:01-01:01:01:03/01:01:01:05-01:02:04/01:04:01:01-01:09/01:11-01:13/01:16N	-, Null	170 bp
E1	E3	E5	E7	E9	E11	Mix 4	DQA1*01:03:01:01-01:03:01:08/01:10/01:14-01:15N	-, Null	170 bp
D1	D3	D5	D7	D9	D11	Mix 5	DQA1*01:04:01:01-01:05:02/01:06?/01:07Q/01:08?-01:09?/01:12?-01:13?/01:15N?, DQA1*02:01:02?, DQA1*03:01:03?, DQA1*04:03N?-04:04?, DQA1*05:02?/05:04?/05:10?, DQA1*06:01:02?-06:02?	-, Null	200 bp
C1	C3	C5	C7	C9	C11	Mix 6	DQA1*02:01:01:01-02:01:02	-	105 bp
B1	B3	B5	B7	B9	B11	Mix 7	DQA1*03:01:01/03:01:03-03:04	-	130 bp
A1	A3	A5	A7	A9	A11	Mix 8	DQA1*04:01:01:01-04:04	-, Null	215 bp
H2	H4	H6	H8	H10	H12	Mix 9	<b>DQA1*05:01:01:01-05:09/05:10w/05:11</b>	-	<b>see below</b>
							DQA1*05:04	-	205 bp
							DQA1*05:01:01:01-05:09/05:10w/05:11	-	190 bp
G2	G4	G6	G8	G10	G12	Mix 10	DQA1*06:01:01:01-06:02	-	105 bp
F2	F4	F6	F8	F10	F12	Mix 11	Negative Control		None (440 bp)

**Well positions:** E2 - A2, E4 - A4, E6 - A6, E8 - A8, E10 - A10, E12 - A12 are empty!

**Amplification control (internal positive control):** 440 base pairs (bp)

**w** = weak

**?** = nucleotide sequence information not available for the primer matching sequence

**Bold:** mixes which result in PCR fragments of different sizes (the specificities are first indicated all in one row, then split into several groups in the subsequent rows depending on the fragment size)

**Table 2:** Amplification patterns of **HLA-DQA1\*** alleles detected by the HLA-DQA1\* CTS-PCR-SSP primer mixes (**Lot No. DQA09-1**) based on IMGT/HLA Sequence Database Release 3.31.0, January 2018

Allele	Serology	1	2	3	4	5	6	7	8	9	10
DQA1*01:01:01:01-01:01:01:03/01:01:01:05-01:01:03	-	1		3							
DQA1*01:02:01:01-01:02:04/01:11/01:16N	-, Null		2	3							
DQA1*01:03:01:01-01:03:01:08/01:10/01:14	-		2		4						
DQA1*01:04:01:01-01:05:02/01:07Q	-	1		3		5					
DQA1*01:06/01:08-01:09/01:13	-		2	3		?					
DQA1*01:12	-	1		3		?					
DQA1*01:15N	Null		2		4	?					
DQA1*02:01:01:01-02:01:01:02	-						6				
DQA1*02:01:02	-					?	6				
DQA1*03:01:01/03:02:01:01-03:04	-							7			
DQA1*03:01:03	-					?		7			
DQA1*04:01:01:01-04:02	-								8		
DQA1*04:03N-04:04	Null, -					?			8		
DQA1*05:01:01:01-05:01:02/05:03:01:01-05:03:01:02/ 05:05:01:01-05:09/05:11	-									9	
DQA1*05:02/05:04	-					?				9	
DQA1*05:10	-					?				w	
DQA1*06:01:01:01-06:01:01:02	-										10
DQA1*06:01:02-06:02	-					?					10

w = weak

? = nucleotide sequence information not available for the primer matching sequence